



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 09:01 am GMT

PDB ID : 1A8M  
Title : TUMOR NECROSIS FACTOR ALPHA, R31D MUTANT  
Authors : Reed, C.; Fu, Z.-Q.; Wu, J.; Xue, Y.-N.; Harrison, R.W.; Chen, M.-J.; Weber, I.T.  
Deposited on : 1998-03-27  
Resolution : 2.30 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

---

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

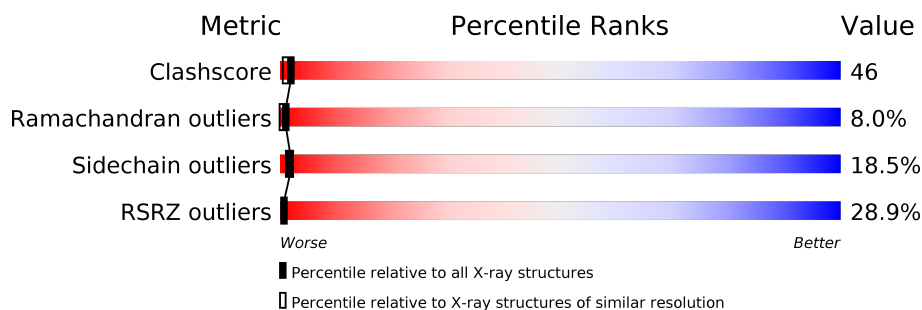
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	157	
1	B	157	
1	C	157	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3630 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called TUMOR NECROSIS FACTOR ALPHA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	152	Total	C	N	O	S	0	0	0
			1187	756	204	225	2			
1	B	152	Total	C	N	O	S	0	0	0
			1187	756	204	225	2			
1	C	152	Total	C	N	O	S	0	0	0
			1187	756	204	225	2			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	ASP	ARG	ENGINEERED	UNP P01375
B	31	ASP	ARG	ENGINEERED	UNP P01375
C	31	ASP	ARG	ENGINEERED	UNP P01375

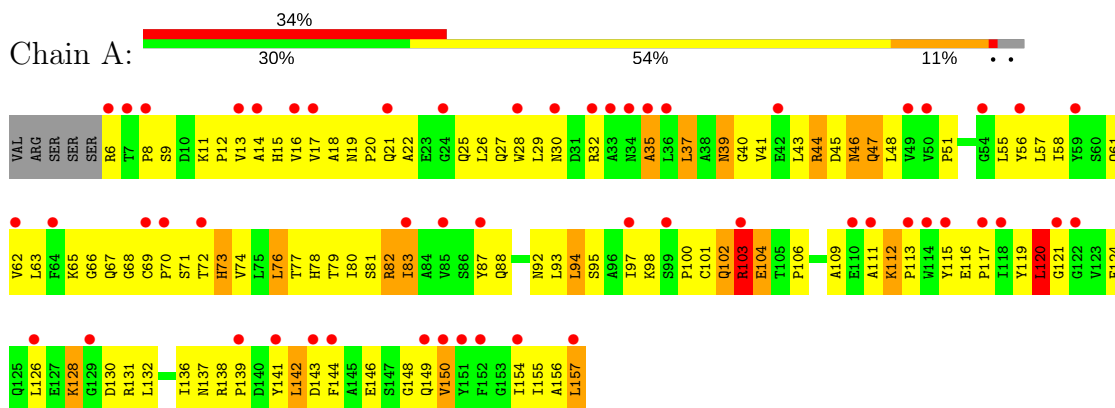
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	16	Total	O	0	0
			16	16		
2	B	25	Total	O	0	0
			25	25		
2	C	28	Total	O	0	0
			28	28		

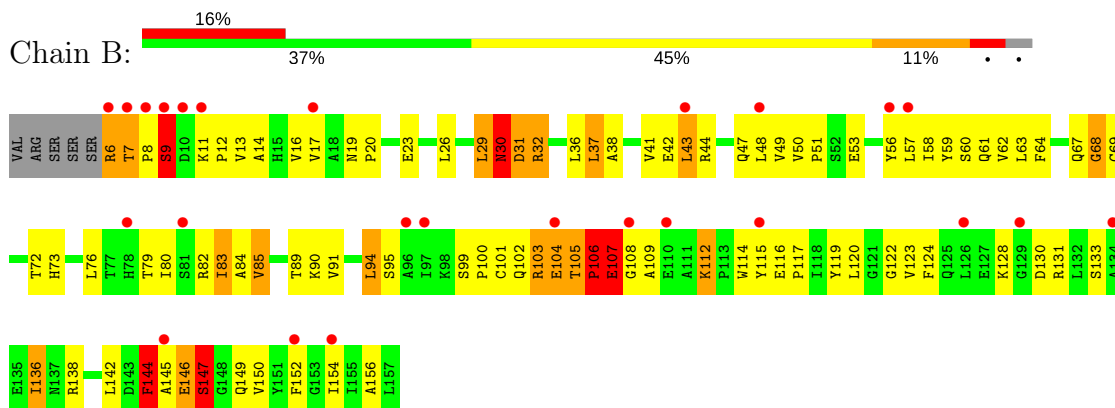
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

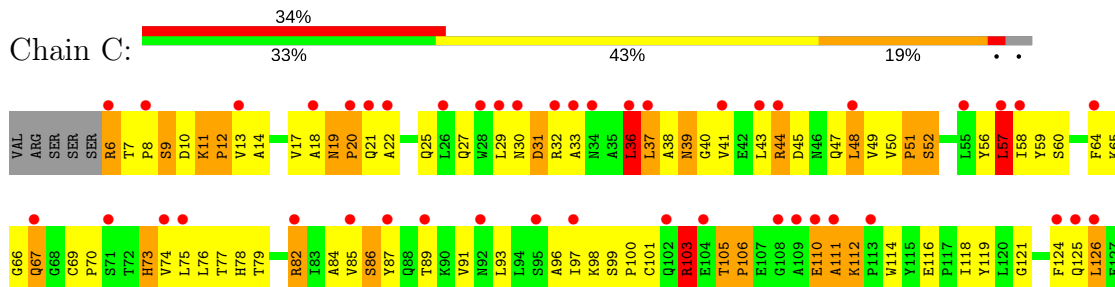
#### • Molecule 1: TUMOR NECROSIS FACTOR ALPHA

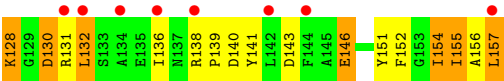


#### • Molecule 1: TUMOR NECROSIS FACTOR ALPHA



#### • Molecule 1: TUMOR NECROSIS FACTOR ALPHA





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	94.70Å 94.70Å 117.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.30 66.96 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.3 (10.00-2.30) 87.9 (66.96-2.30)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.80 (at 2.29Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, $R_{free}$	0.218 , 0.240 0.330 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	33.7	Xtriage
Anisotropy	0.007	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 149.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.82	EDS
Total number of atoms	3630	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.15% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.70	0/1214	1.01	3/1653 (0.2%)
1	B	0.66	0/1214	1.00	4/1653 (0.2%)
1	C	0.64	0/1214	1.01	4/1653 (0.2%)
All	All	0.67	0/3642	1.01	11/4959 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	144	PHE	N-CA-C	8.10	132.86	111.00
1	A	157	LEU	CA-CB-CG	7.73	133.08	115.30
1	B	147	SER	N-CA-C	-6.56	93.30	111.00
1	C	37	LEU	N-CA-C	-6.50	93.46	111.00
1	A	120	LEU	CA-CB-CG	5.92	128.91	115.30
1	C	57	LEU	CA-CB-CG	5.73	128.48	115.30
1	B	145	ALA	N-CA-C	-5.63	95.80	111.00
1	C	36	LEU	CA-CB-CG	5.61	128.19	115.30
1	A	102	GLN	N-CA-C	-5.47	96.23	111.00
1	B	30	ASN	N-CA-C	-5.35	96.57	111.00
1	C	40	GLY	N-CA-C	5.17	126.03	113.10

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1187	0	1178	146	1
1	B	1187	0	1178	100	2
1	C	1187	0	1178	101	0
2	A	16	0	0	4	1
2	B	25	0	0	5	0
2	C	28	0	0	9	0
All	All	3630	0	3534	320	2

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 46.

All (320) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:LYS:HB3	1:A:112:LYS:HZ2	1.26	1.00
1:C:11:LYS:HB2	2:C:266:HOH:O	1.61	1.00
1:A:11:LYS:HD2	1:A:12:PRO:HD2	1.42	0.96
1:A:112:LYS:HB3	1:A:112:LYS:NZ	1.88	0.88
1:A:149:GLN:HG2	1:A:150:VAL:HG12	1.56	0.87
1:C:58:ILE:HD12	1:C:124:PHE:HD2	1.36	0.87
1:C:19:ASN:HB2	1:C:29:LEU:HD12	1.57	0.87
1:C:52:SER:HA	1:C:128:LYS:HB2	1.55	0.86
1:C:20:PRO:HD3	1:C:32:ARG:NH1	1.93	0.83
1:A:128:LYS:NZ	1:A:128:LYS:HB2	1.91	0.82
1:B:79:THR:HG22	1:B:95:SER:HB2	1.60	0.82
1:A:14:ALA:HB2	1:A:41:VAL:HG11	1.60	0.81
1:C:7:THR:HB	2:C:260:HOH:O	1.80	0.81
1:B:26:LEU:HD22	1:B:136:ILE:HD12	1.65	0.79
1:A:15:HIS:O	1:A:35:ALA:HA	1.83	0.78
1:A:12:PRO:HB3	1:A:39:ASN:O	1.83	0.78
1:B:61:GLN:HA	2:B:224:HOH:O	1.82	0.77
1:A:13:VAL:HG12	1:A:155:ILE:HA	1.64	0.77
1:C:69:CYS:SG	1:C:101:CYS:CB	2.72	0.77
2:B:262:HOH:O	1:C:36:LEU:HD23	1.84	0.77
1:B:146:GLU:O	1:B:147:SER:HB2	1.86	0.76
1:C:58:ILE:HD12	1:C:124:PHE:CD2	2.20	0.76
1:A:63:LEU:HD12	1:A:149:GLN:HG3	1.67	0.76
1:B:12:PRO:HG2	1:B:156:ALA:HB2	1.68	0.75
1:A:76:LEU:HD22	1:A:100:PRO:HD3	1.70	0.73
1:A:112:LYS:HE3	1:C:103:ARG:HB2	1.69	0.73
1:C:82:ARG:HH11	1:C:84:ALA:HB2	1.54	0.73
1:C:76:LEU:HD13	2:C:234:HOH:O	1.88	0.72

*Continued on next page...*



*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:100:PRO:HB3	1:B:116:GLU:HG3	1.70	0.72
1:A:98:LYS:HD3	1:A:116:GLU:OE1	1.89	0.72
1:B:47:GLN:HG2	1:B:133:SER:HB3	1.72	0.71
1:B:136:ILE:HD13	1:B:136:ILE:H	1.53	0.71
1:B:124:PHE:HA	2:C:242:HOH:O	1.90	0.71
1:B:69:CYS:CB	1:B:101:CYS:HG	2.04	0.71
1:A:11:LYS:HD2	1:A:12:PRO:CD	2.21	0.71
1:B:32:ARG:HH11	1:B:32:ARG:HG3	1.53	0.71
1:C:69:CYS:SG	1:C:101:CYS:HB3	2.32	0.70
1:A:146:GLU:HB2	1:A:149:GLN:HB2	1.74	0.69
1:A:16:VAL:HG11	1:A:43:LEU:HD22	1.73	0.69
1:B:146:GLU:HG3	1:B:147:SER:H	1.57	0.69
1:B:146:GLU:HB3	1:B:149:GLN:HB2	1.73	0.69
1:B:69:CYS:CB	1:B:101:CYS:SG	2.81	0.69
1:A:67:GLN:HA	1:A:113:PRO:HA	1.73	0.69
1:B:26:LEU:HB3	2:B:220:HOH:O	1.91	0.68
1:A:17:VAL:HG12	1:A:35:ALA:HB2	1.75	0.68
1:B:29:LEU:HD23	1:B:32:ARG:HD3	1.74	0.68
1:A:113:PRO:HG2	1:C:73:HIS:HE1	1.58	0.68
1:A:92:ASN:HB2	1:B:147:SER:HB3	1.76	0.67
1:C:103:ARG:HH11	1:C:103:ARG:HB3	1.59	0.67
1:A:32:ARG:HB3	2:A:201:HOH:O	1.94	0.67
1:B:144:PHE:HB2	1:B:146:GLU:HG2	1.75	0.67
1:B:49:VAL:HG22	1:B:131:ARG:HG2	1.76	0.67
1:A:69:CYS:SG	1:A:101:CYS:CB	2.83	0.67
1:A:11:LYS:HB3	1:A:156:ALA:HB3	1.77	0.67
1:A:22:ALA:HB2	1:A:27:GLN:HG3	1.77	0.66
1:C:11:LYS:HB3	1:C:156:ALA:HB3	1.78	0.66
1:C:77:THR:HG22	1:C:97:ILE:HG23	1.77	0.66
1:A:30:ASN:HB3	1:A:37:LEU:HD23	1.77	0.66
1:A:128:LYS:HZ2	1:A:128:LYS:HB2	1.58	0.65
1:B:19:ASN:HB2	1:B:29:LEU:HD13	1.79	0.65
1:A:149:GLN:HG2	1:A:150:VAL:CG1	2.27	0.65
1:A:112:LYS:HD2	1:C:103:ARG:HG3	1.78	0.65
1:A:18:ALA:HB2	1:A:150:VAL:HG22	1.78	0.64
1:B:59:TYR:HA	1:B:120:LEU:O	1.95	0.64
1:C:126:LEU:HD11	1:C:132:LEU:HD21	1.79	0.63
1:A:136:ILE:HD11	1:A:139:PRO:HA	1.80	0.63
1:A:13:VAL:HG12	1:A:155:ILE:HG13	1.79	0.63
1:A:137:ASN:OD1	1:A:138:ARG:HG2	1.99	0.63
1:C:44:ARG:HA	1:C:44:ARG:HE	1.64	0.63

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:LEU:HD11	1:A:150:VAL:HG11	1.81	0.62
1:A:142:LEU:CD1	1:A:150:VAL:HG11	2.29	0.62
1:A:30:ASN:HA	1:A:35:ALA:HB1	1.82	0.62
1:C:50:VAL:HG12	1:C:130:ASP:O	1.99	0.62
1:A:69:CYS:SG	1:A:101:CYS:HB3	2.40	0.62
1:A:93:LEU:O	1:A:94:LEU:HG	2.00	0.62
1:B:16:VAL:HG11	1:B:43:LEU:HD21	1.80	0.62
1:C:87:TYR:HB2	1:C:89:THR:HG22	1.80	0.62
1:B:51:PRO:O	1:B:128:LYS:HG3	2.00	0.61
1:B:30:ASN:O	1:B:31:ASP:HB2	1.99	0.61
1:C:20:PRO:HD3	1:C:32:ARG:HH11	1.64	0.61
1:B:73:HIS:CD2	1:C:112:LYS:HD2	2.36	0.61
1:A:67:GLN:HB3	1:A:111:ALA:HA	1.81	0.60
1:A:112:LYS:HZ2	1:A:112:LYS:CB	2.09	0.60
1:A:71:SER:O	1:A:73:HIS:N	2.34	0.60
1:A:13:VAL:CG1	1:A:155:ILE:HG13	2.31	0.60
1:A:73:HIS:CE1	1:B:112:LYS:HG2	2.37	0.60
1:B:13:VAL:HG22	1:B:14:ALA:N	2.17	0.60
1:C:100:PRO:HA	1:C:116:GLU:OE2	2.01	0.60
1:C:87:TYR:C	1:C:89:THR:H	2.06	0.59
1:B:144:PHE:C	1:B:146:GLU:H	2.05	0.59
1:A:146:GLU:CB	1:A:149:GLN:HB2	2.33	0.58
1:B:59:TYR:H	1:B:59:TYR:HD1	1.51	0.58
1:C:143:ASP:O	1:C:146:GLU:HG3	2.03	0.58
1:A:68:GLY:HA2	1:A:106:PRO:HG3	1.86	0.58
1:C:69:CYS:O	1:C:105:THR:HA	2.03	0.58
1:B:62:VAL:HB	1:B:142:LEU:HD21	1.84	0.58
1:B:20:PRO:HA	1:B:144:PHE:CE1	2.39	0.58
1:C:39:ASN:HD22	1:C:39:ASN:N	2.02	0.58
1:B:146:GLU:CB	1:B:149:GLN:HB2	2.34	0.57
1:B:13:VAL:CG2	1:B:14:ALA:N	2.67	0.57
1:A:41:VAL:HA	1:A:51:PRO:HD3	1.85	0.57
1:A:56:TYR:HE2	2:A:206:HOH:O	1.87	0.57
1:A:80:ILE:O	1:A:93:LEU:HB2	2.05	0.57
1:B:53:GLU:HG2	1:C:8:PRO:HG3	1.86	0.57
1:C:36:LEU:HD21	2:C:242:HOH:O	2.03	0.56
1:B:6:ARG:HE	1:B:6:ARG:N	2.02	0.56
1:A:17:VAL:CG1	1:A:32:ARG:HG3	2.35	0.56
1:A:62:VAL:CG1	1:A:142:LEU:HD21	2.34	0.56
1:A:61:GLN:O	1:A:150:VAL:HA	2.05	0.56
1:B:104:GLU:O	1:B:104:GLU:HG2	2.06	0.56

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:19:ASN:ND2	1:C:22:ALA:HB2	2.21	0.56
1:A:30:ASN:HD22	1:A:37:LEU:HG	1.70	0.56
1:B:146:GLU:HB2	1:B:149:GLN:H	1.71	0.56
1:A:69:CYS:CB	1:A:101:CYS:SG	2.93	0.56
1:B:7:THR:H	1:B:8:PRO:HD2	1.71	0.56
1:A:83:ILE:HG23	1:A:131:ARG:HB2	1.88	0.55
1:A:58:ILE:O	1:A:121:GLY:HA2	2.07	0.55
1:B:144:PHE:CB	1:B:146:GLU:HG2	2.35	0.55
1:C:52:SER:N	1:C:128:LYS:HZ2	2.04	0.55
1:A:14:ALA:CB	1:A:41:VAL:HG11	2.35	0.55
1:C:69:CYS:O	1:C:106:PRO:HD2	2.06	0.55
1:A:82:ARG:CB	1:A:93:LEU:HD11	2.36	0.55
1:B:60:SER:HB3	1:B:80:ILE:HD11	1.89	0.55
1:B:83:ILE:HG22	1:B:90:LYS:HG2	1.90	0.54
1:A:30:ASN:ND2	1:A:37:LEU:HG	2.23	0.54
1:A:40:GLY:O	1:A:51:PRO:HB3	2.07	0.54
1:A:131:ARG:O	1:A:132:LEU:HD12	2.08	0.54
1:B:60:SER:CB	1:B:80:ILE:HD11	2.38	0.54
1:C:41:VAL:HG22	1:C:51:PRO:HD3	1.89	0.54
1:C:43:LEU:HD13	1:C:48:LEU:HD13	1.90	0.54
1:A:69:CYS:H	1:A:106:PRO:HD2	1.72	0.54
1:A:18:ALA:CB	1:A:150:VAL:HG22	2.38	0.54
1:B:69:CYS:O	1:B:105:THR:HA	2.07	0.54
1:A:13:VAL:HG12	1:A:155:ILE:CA	2.38	0.54
1:C:98:LYS:CD	1:C:118:ILE:HG12	2.37	0.54
1:C:66:GLY:HA3	1:C:114:TRP:CE2	2.43	0.53
1:A:57:LEU:HB3	1:A:155:ILE:HG23	1.91	0.53
1:A:17:VAL:HG13	1:A:32:ARG:HG3	1.90	0.53
1:A:6:ARG:HH22	1:C:125:GLN:NE2	2.07	0.53
1:B:20:PRO:HA	1:B:144:PHE:CD1	2.43	0.53
1:B:146:GLU:CG	1:B:147:SER:H	2.18	0.53
1:C:57:LEU:O	1:C:154:ILE:HA	2.09	0.53
1:A:12:PRO:HB2	2:A:206:HOH:O	2.08	0.53
1:A:29:LEU:HD12	1:A:32:ARG:HD3	1.90	0.53
1:B:69:CYS:HG	1:B:101:CYS:HG	0.54	0.53
1:B:16:VAL:CG2	1:B:152:PHE:HB3	2.38	0.53
1:A:58:ILE:HD11	1:A:126:LEU:HD11	1.90	0.52
1:A:138:ARG:NH1	1:A:141:TYR:CE2	2.77	0.52
1:B:82:ARG:NH1	1:B:84:ALA:HB2	2.24	0.52
1:B:69:CYS:HB3	1:B:101:CYS:SG	2.49	0.52
1:C:64:PHE:HE2	1:C:118:ILE:HD12	1.73	0.52

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:136:ILE:HD13	1:B:136:ILE:N	2.23	0.52
1:A:119:TYR:O	1:A:120:LEU:HB3	2.10	0.52
1:A:16:VAL:CG2	1:A:28:TRP:HB3	2.40	0.52
1:C:38:ALA:O	1:C:39:ASN:HB2	2.08	0.52
1:B:123:VAL:HG23	1:C:59:TYR:HE2	1.75	0.52
1:A:103:ARG:HA	1:B:112:LYS:CD	2.40	0.51
1:B:69:CYS:O	1:B:106:PRO:HD2	2.10	0.51
1:B:58:ILE:HG23	1:B:154:ILE:HG22	1.92	0.51
1:A:144:PHE:HA	1:A:149:GLN:HE22	1.75	0.51
1:A:92:ASN:CB	1:B:147:SER:HB3	2.39	0.51
1:A:47:GLN:OE1	1:A:131:ARG:HD3	2.10	0.51
1:C:52:SER:H	1:C:128:LYS:HE3	1.75	0.51
1:A:77:THR:HG22	1:A:97:ILE:HG23	1.92	0.51
1:A:65:LYS:HG2	1:A:66:GLY:N	2.25	0.51
1:A:6:ARG:HH21	1:A:8:PRO:CG	2.23	0.51
1:C:69:CYS:HG	1:C:101:CYS:HG	0.55	0.51
1:B:82:ARG:NH2	1:B:130:ASP:OD2	2.43	0.51
1:C:52:SER:N	1:C:128:LYS:NZ	2.58	0.51
1:B:13:VAL:HG13	1:B:38:ALA:HB3	1.93	0.50
1:A:16:VAL:HG21	1:A:28:TRP:HB3	1.93	0.50
1:B:123:VAL:HG23	1:C:59:TYR:CE2	2.46	0.50
1:C:64:PHE:HA	1:C:141:TYR:O	2.12	0.50
1:C:67:GLN:H	1:C:67:GLN:CD	2.14	0.50
1:A:113:PRO:HG2	1:C:73:HIS:CE1	2.45	0.50
1:A:139:PRO:O	1:A:142:LEU:HB2	2.12	0.50
1:C:14:ALA:HA	1:C:36:LEU:O	2.12	0.49
1:B:119:TYR:HA	2:B:224:HOH:O	2.12	0.49
1:A:112:LYS:CE	1:C:103:ARG:HB2	2.42	0.49
1:C:100:PRO:HB3	1:C:114:TRP:CE3	2.48	0.49
1:C:98:LYS:HD2	1:C:118:ILE:HG12	1.93	0.49
1:B:43:LEU:HD22	1:B:48:LEU:HD23	1.93	0.49
1:A:82:ARG:HB2	1:A:93:LEU:HD11	1.95	0.49
1:A:58:ILE:HG21	1:A:80:ILE:HG21	1.93	0.49
1:A:128:LYS:HZ3	1:A:128:LYS:HB2	1.74	0.49
1:B:37:LEU:HD11	1:B:42:GLU:HA	1.95	0.49
1:B:62:VAL:HA	1:B:150:VAL:HG13	1.94	0.49
1:A:103:ARG:HA	1:B:112:LYS:HD2	1.94	0.48
1:A:146:GLU:HB2	1:A:149:GLN:CB	2.42	0.48
1:C:30:ASN:O	1:C:31:ASP:HB2	2.13	0.48
1:B:67:GLN:O	1:B:68:GLY:O	2.32	0.48
1:A:20:PRO:HD3	1:A:32:ARG:HH11	1.77	0.48

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:102:GLN:HG2	2:B:245:HOH:O	2.14	0.48
1:A:104:GLU:HA	1:B:103:ARG:HH12	1.78	0.48
1:C:60:SER:OG	1:C:78:HIS:HE1	1.97	0.48
1:A:63:LEU:CD2	1:A:117:PRO:HB3	2.44	0.48
1:C:70:PRO:HG3	2:C:238:HOH:O	2.13	0.48
1:C:77:THR:HA	1:C:96:ALA:O	2.13	0.48
1:A:22:ALA:HB1	1:A:25:GLN:HG3	1.94	0.47
1:B:26:LEU:HD13	1:B:142:LEU:CD1	2.44	0.47
1:C:19:ASN:HB2	1:C:29:LEU:CD1	2.38	0.47
1:A:69:CYS:H	1:A:106:PRO:CD	2.27	0.47
1:C:20:PRO:O	1:C:22:ALA:N	2.47	0.47
1:C:51:PRO:CA	1:C:128:LYS:HZ1	2.28	0.47
1:B:107:GLU:C	1:B:109:ALA:H	2.18	0.47
1:A:102:GLN:NE2	1:B:114:TRP:HB3	2.30	0.47
1:B:144:PHE:C	1:B:146:GLU:N	2.68	0.47
1:B:59:TYR:N	1:B:59:TYR:CD1	2.83	0.47
1:B:16:VAL:HG22	1:B:152:PHE:O	2.15	0.47
1:C:77:THR:CG2	1:C:97:ILE:HG23	2.42	0.47
1:C:47:GLN:OE1	1:C:131:ARG:HD3	2.14	0.47
1:B:9:SER:OG	1:B:11:LYS:HG2	2.14	0.47
1:C:155:ILE:HD11	2:C:266:HOH:O	2.13	0.47
1:A:66:GLY:O	1:A:113:PRO:HA	2.15	0.46
1:A:82:ARG:HB3	1:A:93:LEU:HD11	1.97	0.46
1:A:119:TYR:CG	1:A:120:LEU:N	2.83	0.46
1:A:18:ALA:HA	1:A:27:GLN:O	2.14	0.46
1:A:62:VAL:HG12	1:A:63:LEU:N	2.29	0.46
1:C:29:LEU:HD23	1:C:29:LEU:HA	1.69	0.46
1:C:58:ILE:O	1:C:121:GLY:HA2	2.15	0.46
1:A:61:GLN:CD	2:A:236:HOH:O	2.53	0.46
1:B:83:ILE:HG13	1:B:83:ILE:O	2.16	0.46
1:C:65:LYS:NZ	1:C:143:ASP:HA	2.31	0.46
1:A:63:LEU:HD21	1:A:117:PRO:HB3	1.97	0.46
1:A:18:ALA:HB2	1:A:150:VAL:CG2	2.43	0.46
1:A:26:LEU:HD21	1:A:28:TRP:CH2	2.50	0.46
1:A:57:LEU:HB3	1:A:155:ILE:CG2	2.46	0.46
1:B:63:LEU:HD13	1:B:117:PRO:HB3	1.96	0.46
1:C:138:ARG:NH2	1:C:140:ASP:OD2	2.46	0.46
1:C:41:VAL:O	1:C:41:VAL:HG12	2.16	0.46
1:B:13:VAL:CG1	1:B:38:ALA:HB3	2.45	0.45
1:A:102:GLN:O	1:A:104:GLU:N	2.49	0.45
1:A:79:THR:HG22	1:A:95:SER:HB3	1.98	0.45

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:GLU:O	1:B:109:ALA:N	2.49	0.45
1:B:85:VAL:HG23	1:B:130:ASP:OD1	2.16	0.45
1:C:86:SER:OG	1:C:87:TYR:N	2.49	0.45
1:A:69:CYS:CB	1:A:101:CYS:HG	2.26	0.45
1:B:138:ARG:HA	1:B:138:ARG:HD2	1.84	0.45
1:A:119:TYR:CE1	1:C:121:GLY:O	2.70	0.44
1:B:85:VAL:HG21	1:B:128:LYS:O	2.17	0.44
1:A:143:ASP:C	1:A:149:GLN:OE1	2.56	0.44
1:A:76:LEU:HD22	1:A:100:PRO:CD	2.46	0.44
1:C:6:ARG:NH2	1:C:8:PRO:HB3	2.32	0.44
1:B:26:LEU:HD13	1:B:142:LEU:HD13	1.99	0.44
1:C:98:LYS:HD3	1:C:118:ILE:HG12	1.99	0.44
1:A:146:GLU:HB2	1:A:149:GLN:CD	2.38	0.44
1:A:69:CYS:HB3	1:A:101:CYS:HB3	2.00	0.44
1:B:105:THR:O	1:B:106:PRO:O	2.35	0.44
1:A:63:LEU:HA	1:A:63:LEU:HD23	1.82	0.44
1:C:110:GLU:O	1:C:111:ALA:HB3	2.18	0.44
1:C:44:ARG:N	1:C:47:GLN:O	2.50	0.44
1:C:103:ARG:HH11	1:C:103:ARG:CB	2.30	0.43
1:C:30:ASN:HB3	1:C:37:LEU:CD1	2.47	0.43
1:C:82:ARG:NH1	2:C:257:HOH:O	2.50	0.43
1:B:50:VAL:HA	1:B:51:PRO:HD2	1.69	0.43
1:A:100:PRO:O	1:A:101:CYS:HB2	2.18	0.43
1:A:65:LYS:CG	1:A:66:GLY:N	2.80	0.43
1:C:43:LEU:HD12	1:C:47:GLN:C	2.38	0.43
1:C:50:VAL:HG23	1:C:56:TYR:CZ	2.53	0.43
1:A:30:ASN:OD1	1:A:30:ASN:N	2.51	0.43
1:B:144:PHE:O	1:B:146:GLU:HG2	2.18	0.43
1:C:85:VAL:HG11	2:C:258:HOH:O	2.17	0.43
1:C:13:VAL:HB	1:C:155:ILE:HD12	1.99	0.43
1:A:103:ARG:HB2	1:A:104:GLU:H	1.70	0.43
1:A:39:ASN:OD1	1:A:39:ASN:N	2.51	0.43
1:A:148:GLY:HA3	1:C:93:LEU:O	2.18	0.43
1:C:64:PHE:HE2	1:C:118:ILE:CD1	2.32	0.43
1:A:6:ARG:NH2	1:A:8:PRO:HD3	2.34	0.43
1:B:64:PHE:CD2	1:B:76:LEU:HD13	2.54	0.43
1:A:47:GLN:HB3	1:A:132:LEU:O	2.19	0.43
1:A:19:ASN:OD1	1:A:21:GLN:HB3	2.19	0.43
1:B:58:ILE:O	1:B:58:ILE:HG22	2.17	0.43
1:A:44:ARG:C	1:A:46:ASN:H	2.22	0.42
1:C:57:LEU:HB2	1:C:157:LEU:HD22	2.00	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:PRO:HB2	1:A:109:ALA:HB3	2.00	0.42
1:B:83:ILE:HD12	1:B:83:ILE:C	2.40	0.42
1:B:37:LEU:HA	1:B:37:LEU:HD22	1.87	0.42
1:C:52:SER:CA	1:C:128:LYS:HB2	2.37	0.42
1:B:94:LEU:HD23	1:C:151:TYR:CE2	2.55	0.42
1:C:51:PRO:O	1:C:52:SER:OG	2.25	0.42
1:B:37:LEU:HD13	1:B:41:VAL:O	2.20	0.42
1:C:49:VAL:HG22	1:C:131:ARG:HG2	2.01	0.42
1:A:142:LEU:HD22	1:A:142:LEU:HA	1.78	0.42
1:A:62:VAL:HG11	1:A:136:ILE:HG21	2.02	0.42
1:A:102:GLN:HE22	1:B:114:TRP:HB3	1.84	0.42
1:B:115:TYR:C	1:B:116:GLU:HG2	2.40	0.42
1:A:69:CYS:HB3	1:A:101:CYS:SG	2.60	0.42
1:A:22:ALA:CB	1:A:27:GLN:HG3	2.49	0.42
1:B:103:ARG:HG3	1:B:104:GLU:N	2.33	0.42
1:B:50:VAL:HG13	1:B:56:TYR:OH	2.20	0.42
1:A:119:TYR:CE2	1:C:119:TYR:HE1	2.37	0.42
1:C:17:VAL:HG12	1:C:18:ALA:N	2.34	0.42
1:A:137:ASN:O	1:A:138:ARG:HD3	2.20	0.42
1:C:110:GLU:OE2	1:C:111:ALA:HB2	2.20	0.42
1:C:74:VAL:HG23	1:C:74:VAL:O	2.20	0.42
1:A:115:TYR:CE2	1:C:75:LEU:HD22	2.54	0.41
1:C:87:TYR:CB	1:C:89:THR:HG22	2.49	0.41
1:A:16:VAL:CG1	1:A:43:LEU:HD22	2.47	0.41
1:A:82:ARG:HD3	1:A:126:LEU:CD2	2.50	0.41
1:B:13:VAL:CG2	1:B:14:ALA:H	2.33	0.41
1:B:32:ARG:HG3	1:B:32:ARG:NH1	2.29	0.41
1:A:144:PHE:C	1:A:146:GLU:H	2.23	0.41
1:A:113:PRO:CG	1:C:73:HIS:HE1	2.30	0.41
1:A:69:CYS:CB	1:A:101:CYS:HB3	2.51	0.41
1:C:100:PRO:HG2	1:C:114:TRP:CZ3	2.55	0.41
1:A:67:GLN:CB	1:A:111:ALA:HA	2.48	0.41
1:A:82:ARG:NH1	1:A:130:ASP:OD2	2.53	0.41
1:A:58:ILE:O	1:A:121:GLY:CA	2.69	0.41
1:A:136:ILE:CD1	1:A:139:PRO:HA	2.47	0.41
1:A:48:LEU:HD12	1:A:154:ILE:HG23	2.02	0.41
1:B:57:LEU:HA	1:B:122:GLY:O	2.20	0.41
1:A:115:TYR:CD2	1:C:75:LEU:HD22	2.56	0.41
1:A:124:PHE:HA	1:B:36:LEU:HD11	2.03	0.40
1:A:12:PRO:HB2	1:A:51:PRO:HG3	2.03	0.40
1:C:10:ASP:CA	1:C:39:ASN:OD1	2.69	0.40

*Continued on next page...*



Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:73:HIS:CE1	1:B:99:SER:HB2	2.57	0.40
1:C:67:GLN:N	1:C:67:GLN:CD	2.75	0.40
1:A:103:ARG:CA	1:B:112:LYS:HD2	2.52	0.40
1:A:62:VAL:HG23	1:A:78:HIS:CE1	2.57	0.40
1:C:12:PRO:HB2	1:C:56:TYR:HE2	1.86	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:131:ARG:NH2	2:A:212:HOH:O[4_454]	1.82	0.38
1:A:88:GLN:NE2	1:B:31:ASP:O[8_665]	1.90	0.30

## 5.3 Torsion angles

### 5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	150/157 (96%)	108 (72%)	34 (23%)	8 (5%)	2	1
1	B	150/157 (96%)	118 (79%)	19 (13%)	13 (9%)	1	0
1	C	150/157 (96%)	107 (71%)	28 (19%)	15 (10%)	1	0
All	All	450/471 (96%)	333 (74%)	81 (18%)	36 (8%)	1	0

All (36) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	SER
1	A	39	ASN
1	A	72	THR
1	B	31	ASP
1	B	103	ARG
1	B	106	PRO

Continued on next page...



*Continued from previous page...*

Mol	Chain	Res	Type
1	C	9	SER
1	C	20	PRO
1	C	21	GLN
1	C	33	ALA
1	C	103	ARG
1	C	112	LYS
1	A	70	PRO
1	B	68	GLY
1	B	108	GLY
1	C	31	ASP
1	C	51	PRO
1	C	73	HIS
1	C	111	ALA
1	C	146	GLU
1	A	35	ALA
1	A	103	ARG
1	A	104	GLU
1	B	85	VAL
1	B	146	GLU
1	C	86	SER
1	A	120	LEU
1	B	7	THR
1	B	72	THR
1	B	107	GLU
1	B	9	SER
1	B	105	THR
1	B	112	LYS
1	C	11	LYS
1	C	52	SER
1	C	105	THR

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	128/133 (96%)	107 (84%)	21 (16%)	<b>2</b> <b>2</b>

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	128/133 (96%)	108 (84%)	20 (16%)	3	3
1	C	128/133 (96%)	98 (77%)	30 (23%)	1	0
All	All	384/399 (96%)	313 (82%)	71 (18%)	2	1

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	37	LEU
1	A	44	ARG
1	A	45	ASP
1	A	46	ASN
1	A	47	GLN
1	A	55	LEU
1	A	73	HIS
1	A	74	VAL
1	A	76	LEU
1	A	81	SER
1	A	82	ARG
1	A	83	ILE
1	A	87	TYR
1	A	94	LEU
1	A	103	ARG
1	A	112	LYS
1	A	120	LEU
1	A	128	LYS
1	A	142	LEU
1	A	150	VAL
1	A	157	LEU
1	B	6	ARG
1	B	9	SER
1	B	17	VAL
1	B	23	GLU
1	B	29	LEU
1	B	30	ASN
1	B	32	ARG
1	B	37	LEU
1	B	43	LEU
1	B	44	ARG
1	B	83	ILE
1	B	89	THR
1	B	91	VAL

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	B	94	LEU
1	B	104	GLU
1	B	106	PRO
1	B	107	GLU
1	B	136	ILE
1	B	144	PHE
1	B	147	SER
1	C	6	ARG
1	C	9	SER
1	C	12	PRO
1	C	19	ASN
1	C	25	GLN
1	C	27	GLN
1	C	36	LEU
1	C	39	ASN
1	C	44	ARG
1	C	45	ASP
1	C	48	LEU
1	C	57	LEU
1	C	67	GLN
1	C	79	THR
1	C	82	ARG
1	C	91	VAL
1	C	99	SER
1	C	103	ARG
1	C	106	PRO
1	C	110	GLU
1	C	126	LEU
1	C	128	LYS
1	C	130	ASP
1	C	132	LEU
1	C	136	ILE
1	C	139	PRO
1	C	152	PHE
1	C	154	ILE
1	C	155	ILE
1	C	157	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	46	ASN
1	A	61	GLN
1	A	67	GLN
1	A	92	ASN
1	B	73	HIS
1	B	92	ASN
1	B	149	GLN
1	C	61	GLN
1	C	73	HIS
1	C	78	HIS
1	C	92	ASN

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	152/157 (96%)	1.90	54 (35%) 0 0	10, 36, 81, 91	0
1	B	152/157 (96%)	1.21	25 (16%) 2 3	12, 31, 77, 108	0
1	C	152/157 (96%)	1.82	53 (34%) 0 0	16, 35, 77, 91	0
All	All	456/471 (96%)	1.64	132 (28%) 1 1	10, 34, 79, 108	0

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	108	GLY	11.2
1	C	87	TYR	7.6
1	C	6	ARG	7.3
1	A	32	ARG	6.3
1	C	33	ALA	6.3
1	C	8	PRO	6.0
1	A	34	ASN	5.8
1	B	56	TYR	5.8
1	A	103	ARG	5.6
1	A	50	VAL	5.6
1	A	72	THR	5.4
1	B	7	THR	5.4
1	C	26	LEU	5.2
1	A	35	ALA	5.1
1	A	111	ALA	5.0
1	A	6	ARG	4.9
1	B	129	GLY	4.6
1	B	8	PRO	4.4
1	C	97	ILE	4.3
1	C	36	LEU	4.1
1	C	144	PHE	4.1
1	C	136	ILE	4.0
1	A	16	VAL	3.9

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	83	ILE	3.9
1	C	157	LEU	3.9
1	A	36	LEU	3.9
1	A	121	GLY	3.8
1	A	7	THR	3.8
1	C	71	SER	3.8
1	B	108	GLY	3.7
1	A	144	PHE	3.6
1	A	118	ILE	3.6
1	A	157	LEU	3.5
1	A	42	GLU	3.5
1	A	110	GLU	3.5
1	C	32	ARG	3.5
1	A	115	TYR	3.5
1	B	11	LYS	3.4
1	A	87	TYR	3.4
1	C	109	ALA	3.3
1	C	28	TRP	3.2
1	A	64	PHE	3.2
1	A	114	TRP	3.2
1	C	20	PRO	3.2
1	A	33	ALA	3.1
1	A	85	VAL	3.1
1	A	49	VAL	3.1
1	C	30	ASN	3.1
1	C	142	LEU	3.1
1	A	69	CYS	3.1
1	A	150	VAL	3.0
1	C	41	VAL	3.0
1	A	122	GLY	3.0
1	A	152	PHE	3.0
1	A	129	GLY	3.0
1	B	10	ASP	3.0
1	A	151	TYR	2.9
1	B	115	TYR	2.9
1	C	48	LEU	2.9
1	C	126	LEU	2.9
1	C	29	LEU	2.9
1	B	6	ARG	2.9
1	C	134	ALA	2.8
1	C	85	VAL	2.8
1	C	102	GLN	2.8

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	A	30	ASN	2.8
1	C	111	ALA	2.8
1	A	8	PRO	2.8
1	A	126	LEU	2.8
1	B	126	LEU	2.8
1	C	37	LEU	2.8
1	C	89	THR	2.7
1	A	70	PRO	2.7
1	A	56	TYR	2.7
1	B	57	LEU	2.7
1	A	13	VAL	2.6
1	B	154	ILE	2.6
1	C	58	ILE	2.6
1	A	21	GLN	2.6
1	A	28	TRP	2.6
1	C	55	LEU	2.6
1	B	152	PHE	2.6
1	C	34	ASN	2.6
1	A	149	GLN	2.5
1	A	143	ASP	2.5
1	C	92	ASN	2.5
1	C	44	ARG	2.5
1	A	97	ILE	2.5
1	A	14	ALA	2.4
1	C	13	VAL	2.4
1	A	24	GLY	2.4
1	C	132	LEU	2.4
1	A	54	GLY	2.4
1	A	59	TYR	2.4
1	A	141	TYR	2.4
1	C	131	ARG	2.4
1	B	96	ALA	2.3
1	A	17	VAL	2.3
1	C	64	PHE	2.3
1	A	113	PRO	2.3
1	C	18	ALA	2.3
1	B	43	LEU	2.3
1	C	75	LEU	2.3
1	C	74	VAL	2.2
1	A	139	PRO	2.2
1	C	95	SER	2.2
1	C	124	PHE	2.2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	RSRZ
1	B	9	SER	2.2
1	B	110	GLU	2.2
1	B	17	VAL	2.2
1	A	99	SER	2.2
1	C	67	GLN	2.2
1	A	62	VAL	2.2
1	C	21	GLN	2.2
1	C	125	GLN	2.2
1	C	113	PRO	2.2
1	B	104	GLU	2.2
1	C	57	LEU	2.1
1	C	138	ARG	2.1
1	B	78	HIS	2.1
1	B	48	LEU	2.1
1	C	82	ARG	2.1
1	B	134	ALA	2.1
1	B	145	ALA	2.1
1	C	43	LEU	2.1
1	C	110	GLU	2.1
1	C	22	ALA	2.1
1	A	154	ILE	2.0
1	B	97	ILE	2.0
1	C	104	GLU	2.0
1	A	117	PRO	2.0
1	B	81	SER	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

There are no ligands in this entry.



## 6.5 Other polymers [i](#)

There are no such residues in this entry.